

FIG.1

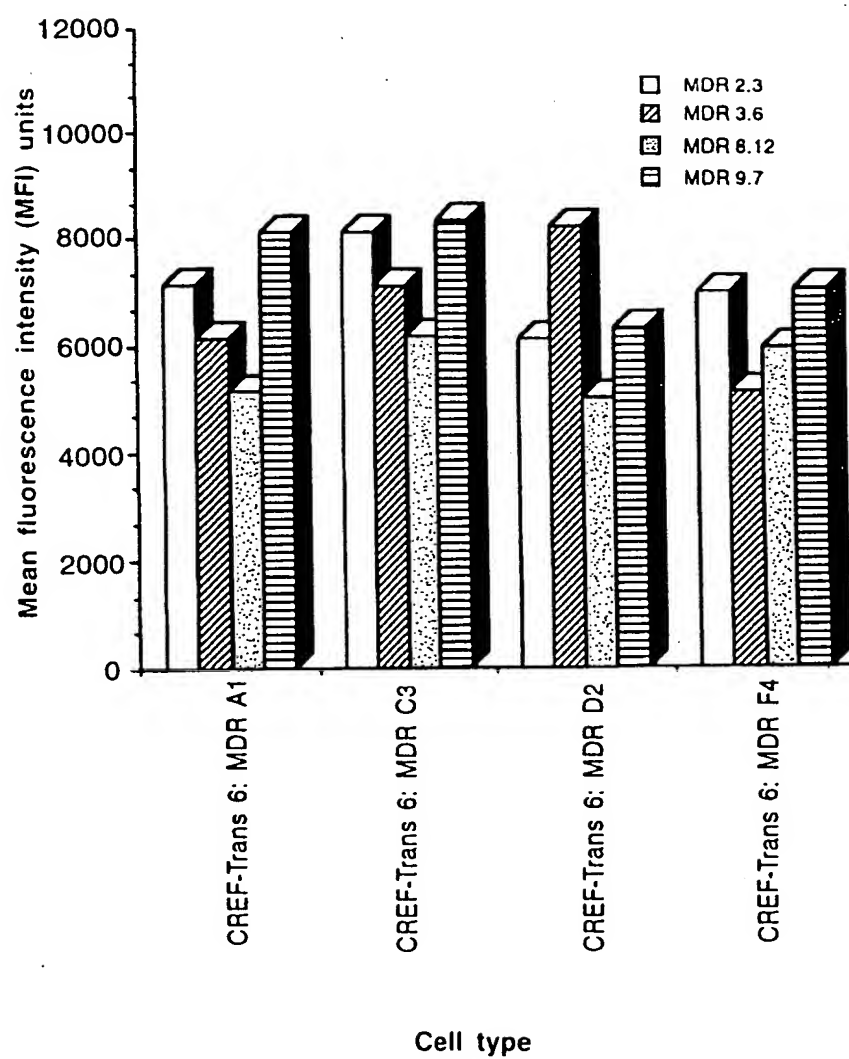


FIG.2

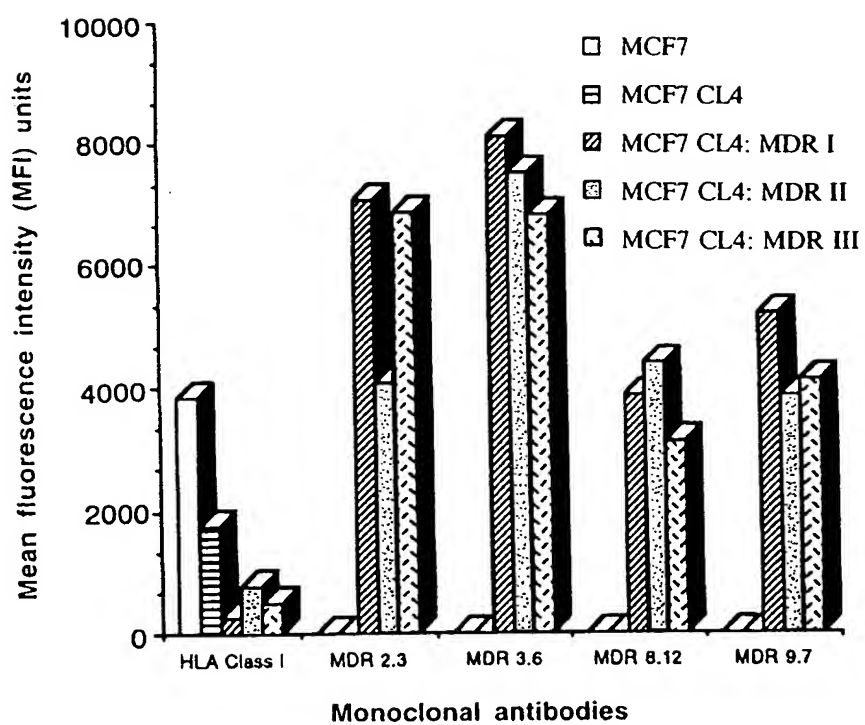


FIG.3

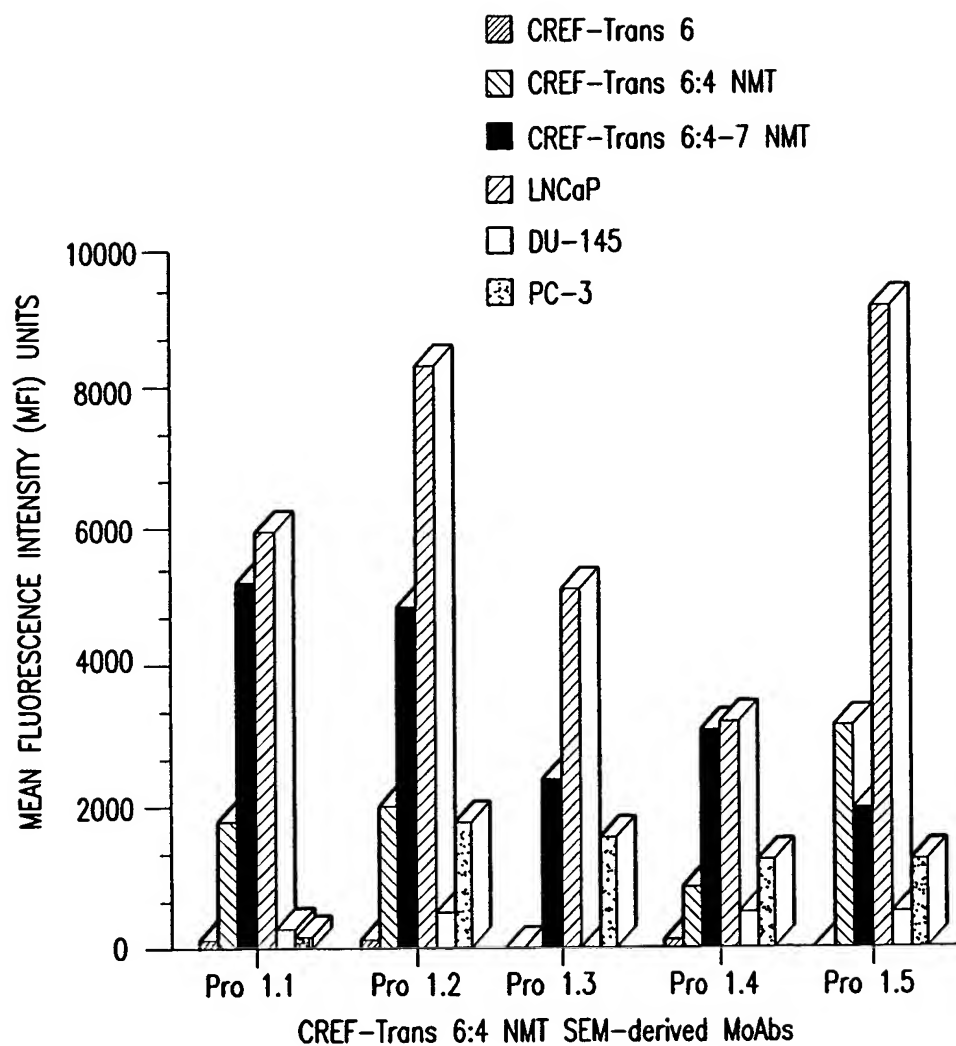


FIG.4

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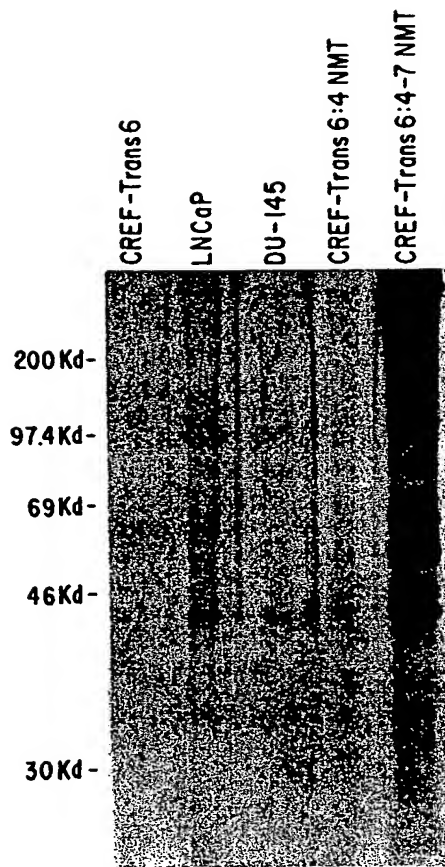


FIG.5

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CREF-Trans 6  
CREF-Trans 6: 4 NMT



FIG.6

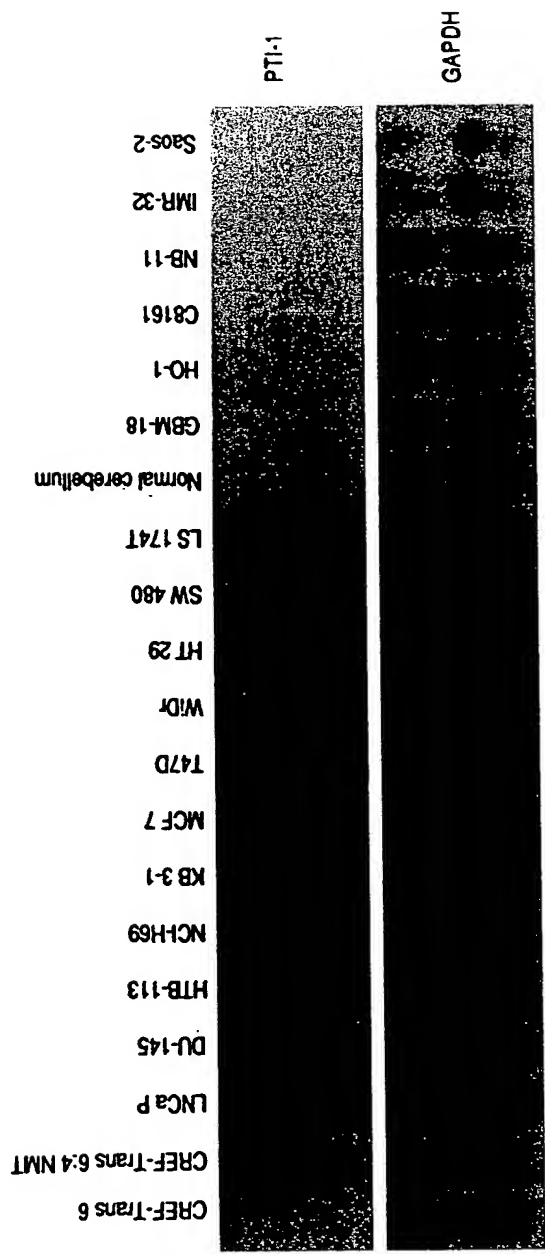


FIG. 7







(E)1		MGKEKTHINIVVIGH	15
(E)16	<u>VDSGKSTTIIGHLIVKCGGIDKRTDEKEKEAAEMGKSEKYAWVLDKLKAER</u>		67
(P)1		MQS	3
(E)68	ERGITIDISLWKFETSKYYVTIIDAPGHRDFIKNNMITGTSQADCAVLIVAAGV	*	120
(P)4	ERGITIDISLWKFETSKYYVTIIDAPGHRDFIQNNMITGTSQADCAVLIVAAGV		56
(E)121	GEFEAGISKNGQITREHALLAYTLGVKQLIVGVNKMMDSTEPPYSQKRYEEIVKE		173
(P)57	GEFEAGISKNGQITREHALLAYTLGVKQLIVGVNKMMDSTEPPYSQKRYEEIVKE		109
(E)174	VSTYTKKIGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGN		223
(P)110	VSTYTKKIGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGN		159
(E)224	SGTTLLEALDCILPPTRPDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGM	*	276
(P)160	SGTTLLEALDCILPPTRPDKPLGLPLQDVYKIGGIGTVPVGRVETGVLKPGM		212
(E)277	VVTFAPVNVTTIEVKSVEMHHEALSEALPGDNVGFNVKNVSVKDVRRGNV	*	325
(P)213	VVTFGPVNVTTIEVKSVEMHHEALGEALPGDNVGFNVKNVSVKDVRRGNV		261
(E)326	AGDSKNDPPMEAAAGFTAQVILNHPGQISAGYAPVLDCHTAHACKFAELK	*	376
(P)262	AGDSKNDPPMEAAAGFPAQVILNHPGQISAGYAPVLDCHTAHACKFAELK		312
(E)377	EKIDRRSGKKLEDGPKFLKSGDAAIVDMVPKPMCVESFSDYPPLGRFAVRD	*	428
(P)313	EKIDRRSGKKLEDGPKFLKSGDAAIVDMVPKPMCVESFSDYPPLGCFAVRD		364
(E)429	MRQTVAVGVKAVDKKAAGAGKVTKSAQKAQKAK		462
(P)365	MRQTVAVGVKAVDKKAAGAGKVTKSAQKAQKAK		398

FIG.8C

Human EF-1 $\alpha$	Amino Acid	K (100)	R (247)	A (281)	S (300)	T (341)	R (423)
	Codon	AAA	CGC	GCT	AGT	ACT	CGC
	Nucleotide	A	C	C	A	A	C
PTI-1	Amino Acid	Q (36)	G (183)	G (217)	G (236)	P (277)	C (359)
	Codon	CAA	GGC	GGT	GGT	CGT	TGC
	Nucleotide	C	G	G	G	C	T

FIG.8D

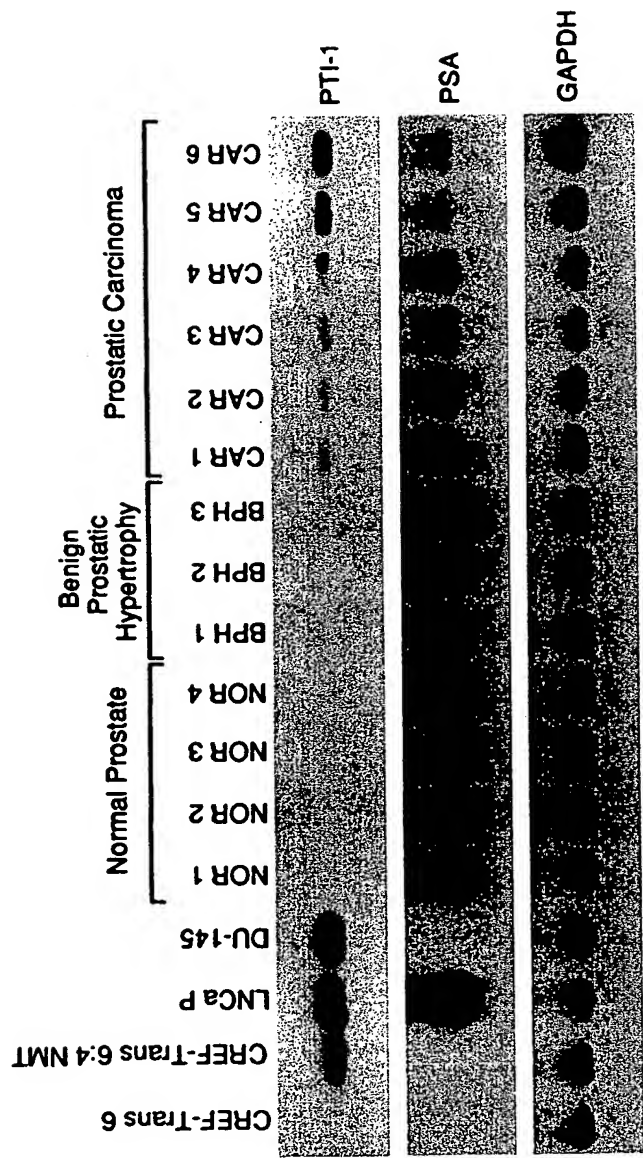


FIG.9

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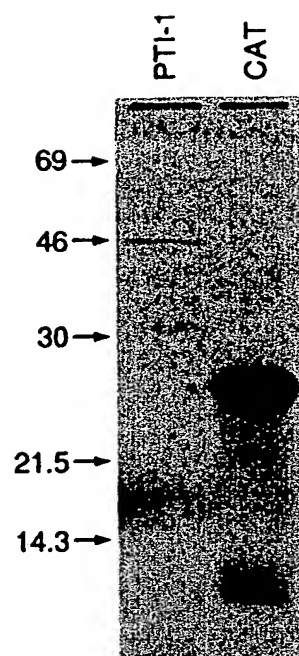


FIG.10

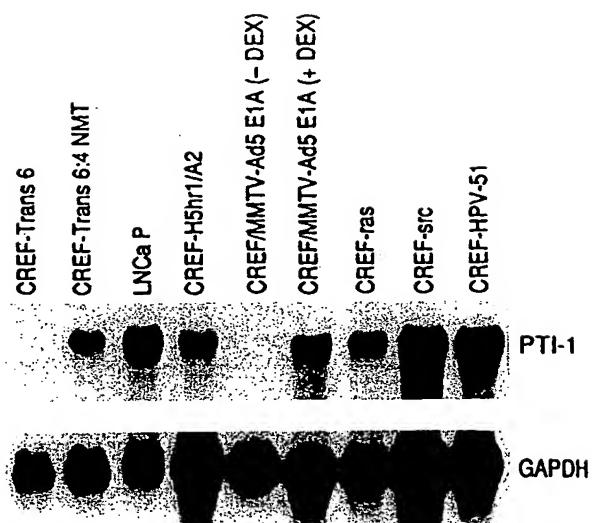


FIG.11

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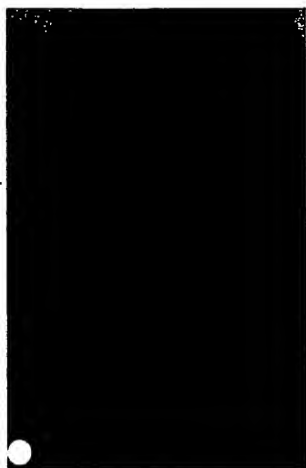


FIG. 12A



FIG. 12B



FIG. 12C



FIG. 12D

1 CGGACCGAGC TCCGTTGCAT TTTGATGAAT CCATAGTCAA ATTAGCGAGA  
 51 CACGTTGCGA ATTGAAACAT CTTAGTAGCA ACAGGAAAAG AAAATAAATA  
 101 ATGATTTCGT CAGTAGTGGC GAGCGAAAGC GAAAGAGCCC AAACCTGTAA  
 151 AGGGGGGTTG GTAGGACATC TTACATTGAG TTACAAAATT TTATGATAGT  
 201 AGAAGAAGTT GGGAAAGCTT CAACATAGAA GGTGATATTC CTGTATACGA  
 251 AATCATAAAA TCTCATAGAT GTATCCTGAG TAGGGCGGGG TACGTGAAAC  
 301 CCTGTCTGAA TCTGCCCGGG ACCACCCGTA AGGCTAAATA CTAATCAGAC  
 351 ACCGATAGTG AACTAGTACC GTGAGGGAAA GGTGAAAAGA ACCCGAGAGG  
 401 GGAGTGAAAT AGATTCTGAA ACCATTTACT TACAAGTAGT CAGAGCACGT  
 451 TAAAGTGTGA TGGCGTACAT CTTGCAGTAT GGGCCGGCGA GTTATGTTAA  
 501 TATGCAAGGT TAAGCACGAA AAAAGCGGAG CCGTAGGGAA ACCGAGTCTG  
 551 AATAGGGCGA CTTTAGTATA TTGGCATATA CCCGAAACCA GGTGATCATC  
 601 CATGAGCAGG TTGAAGCTTA GGTAAACTA AGTGGAGGAC CGAACCCTAG  
 651 TACGCTAAAA AGTGCCCGGA TGACTTGTGG ATAGTGGTGA AATTCCAATC  
 701 GAACCTGGAG ATAGCTGGTT CTCTTCGAAA TAGCTTTAGG GCTAGCGTAT  
 751 AGTACTGTTT AATGGGGGTA GAGCACTGAA TGTGGAATGG CGGCATCTAG  
 801 CTGTACTGAC TATAATCAAA CTCCGAATAC CATTAAAAATT AAGCTATGCA  
 851 GTCGGAACGT GGGTGATAAC GTCCACGCTC GCGAGGGAAA CAACCCAGAT  
 901 CCGTCAGCTA AGGTCCCAAA ATTGTGTTAA GTGAGAAAGG TTGTGGAGAT  
 951 TTCATAAACA ACTAGGAAGT TGGTTTAGAA GCAGCCACCT TTAAAGAGT  
 1001 GCGTAATTGC TCACTAGTCA AGAGATCTTG CGCCAATAAT GTAACGGGAC  
 1051 TCAAACACAA TACCCAAGCT ACGGGCACAT TATGTGCGTT AGGAGAGCGT  
 1101 TTTAATTTCTG TTGAAGTCAG ACCGTGAGAC TGGTGGAGAG ATTAAAAAGTT  
 1151 CGAGAATGCC GGCATGAGTA ACGATTGAA GTGAGAATCT TCGACGCCTA  
 1201 TTGGGAAAGG TTTCCTGGGC AAGGTTCTCC ACCCAGGGTT AGTCAGGGCC  
 1251 TAAGATGAGG CAGAAATGCA TAGTCGATGG ACAACAGGTT AATATTCCTG

FIG.13A

1301 TACTTGGTAA AAGAATGATG GAGTGACGAA AAAGGATAGT TCTACCACTT  
1351 CCACTATGTC CTATCAATAG GAGCTGTATT TGGCATCATA GGAGGCTTCA  
1401 TTCACTGATT TCCCCTATTC TCAGGCTACA CCCTAGACCA AACCTACGCC  
1451 AAAATCCATT TCACTATCAT ATTCATCGGC GTAAATCTAA CTTTCTTCCC  
1501 ACAACACTTT CTCGGCCTAT CCGGAATGAC CCGACCCGAC GTTACTCGGA  
1551 CTACCCCGAT GCATACACCA CATGAAACAT CCTATCATCT GTAGGCTCAT  
1601 TCATTTCTCT AACAGCAGTA ATATTAATAA TTTTCATGAT TTGAGAAGCC  
1651 TTCGCCTTCG AAGCGAAAAG TCCTAATAGT AGAAGAACCC TCCATAAACC  
1701 TGGAGTGACT ATATGGATGC CCCCACCCTA CCTCACATTC GAAGAACCCG  
1751 TATACATAAA ATCTAGACAA AAAAGGAAGG AAGTGAACGC CCCACAAAAA  
1801 AAAAAAAAAA AAAAAAAAAA

**FIG.13B**



1 AACTAAGTGG AGGACCGAAC CGTAGTACGC TAAAAAGTGC CCGGATGACT  
 51 TGTGGATAGT GGTGAAATTC CAATCGAACC TGGAGATAGC TGGTTCCTT  
 101 CGAAATAGCT TTAGGGCTAG CGTATAGTAT TGTTTAATGG GGGTAGAGCA  
 151 CTGAATGTGG AATCGGCGGC ATCTAGCTGT ACTGACTATA ATCAAACCTC  
 201 GAATACCATT AAAATTAAGC TATGCAGTCG GAACGTGGGT GATAACCTCC  
 251 ACTCTCGCGA GGGAAACAAC CCAGATCGTC AGCTAAGGTC CAAAAATTGT  
 301 GTTAAGTGAG AAAGGTTGTG AGATTTCATA AACAACTAGG AAGTTGGCTT  
 351 AGAAGCAGCC ACCTTTTAAA GAGTGCCTAA TTGCTCACTA GTCAAGAGAT  
 401 CTTGCGCCAA TAATGTAACG GGA CTCAAAC ACAATACCGA AGCTACGGGC  
 451 ACATTATGTC GGTTAGGAGA GCGTTTAAAT TTCGTTGAAG TCAGACCGTG  
 501 AGACTGGTGG AGAGATTAAA AGTTCGAGAA TGCCCGGCAT GAGTAACGAT  
 551 TCGAAGTGAG AATCTTCGAC GCCTATTGGG AAAGGTTTCC TGGGCAAGGT  
 601 TCGTCCACCC AGGGTTAGTC AGGGCCTAAG ATGAGGCAGA AATGCATAGT  
 651 CGATGGACAA CAGGTTAATA TTCCTGTACT TGGTAAAAGA ATGATGGAGT  
 701 GACGAAAAAG GATAGTTCTA CCACTTACTG GATTGTGGGG TAAGCAACAA  
 751 GAGAGTTATA TAGGCAAATC CGTATAGCAT AATCTTGAGT TGTGATGCAT  
 801 AGTGAAGACT TCGGTCGAGT AACGAATTGA ATCGATTTC TGTTCGAAG  
 851 AAAAGCTTCT AGTGTTAATT TTTTATCAAC CTGTACCGAG AACGAACACA  
 901 CGTTCCCAAG ATGAGTATTC TAAGGCGAGC GAGAAAACCA ATGTTAAGGA  
 951 ACTCTGCAA ATAACCCCGT AAGTTCGCGA GAAGGGGCGC CTATTTTAA  
 1001 TAGGCCACAG AAAATAGGGG GGCAACTGTT TATCAAAAAC ACAGCTCTCT  
 1051 GCTAAGTTGT AAAACGACGT ATAGAGGGTG AAGCCTGCCC AGTCCCGAAG  
 1101 TTAAACGGAG ATGTTAGCTT ACGCAAAGCA TTAAAGTGAA GCCCGGGTGA  
 1151 ACGGCGGCCG TAACTATAAC GGTCTAAGG TAGCGAAAT CCTTGTCAAC  
 1201 TAATTATTGA CCTGCACGAA AGGCGCAATG ATCTCCCTAC TGTCTCAACA  
 1251 TTGGA CTGG TGA AATTATG GTACCA GTGA AAACGCAGGT TACCCGCATC

FIG. 14A

1301 AAGACGAAAA GACCCCGTGG AGCTTTACTA TAACTTCGTA TTGAAAATTG  
1351 GTTTAGCATG TGTAGGATAG GCGGGAGACT TTGAAGCTGG GACGCTAGTT  
1401 CTAGTGGAGT CAACCTTGAA ATACCACCCT TGCTAAATTG ATTTTCTAAC  
1451 CCGTTCCCCT TATCTGGAAG GAGACAGTGC GTGGTGGGTA GTTTGACTGG  
1501 GCGGTCGCCT CCTAAAGTGT AACGGAGGCG TTCAAAGCTA CACTCAATAT  
1551 GGTCAGAAAC CATATGCAGA GCACAAAGGT AAAAGTGTGG TTGACTGCAA  
1601 GACTTACAAG TCGAGCAGGT GCGAAAGCAG GACTTAGTGA TCCGGCCGTA  
1651 CATTGTGGAA TGGCCGTCGC TCAACGGATA AAAGTCACCC CGGGGATAAC  
1701 AGGCTAATCT TCCCAAGAG ATCACATCGA CGGGAAGGTT TGGCACCTCG  
1751 ATGTCGGCTC ATCGCATCCT GGAGCTGGAG TCGGTTCCAA GGGTTTGCTG  
1801 TTCGCCAATT AAAGCGGTAC GTGAGCTGGG TTCAGAACGT CGTGAGACAG  
1851 TTCGGTCCTC CACTTAGTT

**FIG.14B**

- 1 CGGCACGAGC GGCACGAGAG AAGAGACTCC AATCGACAAG  
AAGCTGAAAA
- 51 AGAATGATGT TGCCTTAAA CAACCTACAG AATATCATCT  
ATAACCCGGT
- 101 AATCCCGTTT GTTGGCACCA TTCCTGATCA GCTGGATCCT  
GGAACCTTGA
- 151 TTGTGATACG TGGGCATGTT CCTAGTGACG CAGACAGATT  
CCAGGTGGAT
- 201 CTGCAGAATG GCAGCAGCGT GAAACCTCGA GCCGATGTGG  
CCTTTCATTT
- 251 CAATCCTCGT TTCAAAAGGG CCGGCTGCAT TGTTTGCAAT  
ACTTTGATAA
- 301 ATGAAAAATG GGGACGGGAA GAGATCACCT ATGACACGCC  
TTTCAAAAGA
- 351 GAAAAGTCTT TTGAGATCGT GATTATGGTG CTGAAGGACA  
AATTCCAGGT
- 401 GGCTGTAAAT GGAAAACATA CTCTGCTCTA TGGCCACAGG  
ATCGGCCAG
- 451 AGAAAATAGA CACTCTGGGC ATTTATGGCA AAGTGAATAT  
TCACTCAATT
- 501 GGTTTTAGCT TCAGCTCGGA CTTACAAAGT ACCCAAGCAT  
CTAGTCTGGA
- 551 ACTGACAGAG ATAGTTAGAG AAAATGTTCC AAAGTCTGGC  
ACGCCCCAGC
- 601 TTAGCCTGCC ATTCGCTGCA AGGTGAACA CCCCATGGG  
CCCTGGACGA
- 651 ACTGTCGTCG TTCAAGGAGA AGTGAATGCA AATGCCAAAA  
GCTTTAATGT
- 701 TGACCTACTA GCAGGAAAAT CAAAGGATAT TGCTCTACAC  
TTGAACCCAC
- 751 GCCTGAATAT TAAAGCATTG GTAAGAAATT CTTTCTTCA  
GGAGTCCTGG
- 801 GGAGAAGAAG AGAGAAATAT TACCTCTTTC CCATTTAGTC  
CTGGGATGTA

FIG.15A

- 851 CTTTGAGATG ATAATTTATT GTGATGTTAG AGAATTCAAG  
GTTGCAGTAA
- 901 ATGGCGTACA CAGCCTGGAG TACAAACACA GATTTAAAGA  
GCTCAGCAGT
- 951 ATTGACACGC TGGAAATTAA TGGAGACATC CACTTACTGG  
AAGTAAGGAG
- 1001 CTGGTAGCCT ACCTACACAG CTGCTACAAA AACCAAAATA  
CAGAATGGCT
- 1051 TCTGTGATAC TGGCCTTGCT GAAACGCATC TCACTGGTCA  
TTCTATTGTT
- 1101 TATATTGTTA AAATGAGCTT GTGCACCATT AGGTCCTGCT  
GGGTGTTCTC
- 1151 AGTCCTTGCC ATGACGTATG GTGGTGTCTA GCACTGAATG  
GGGAAACTGG
- 1201 GGGCAGCAAC ACTTATAGCC AGTTAAAGCC ACTCTGCCCT  
CTCTCCTACT
- 1251 TTGGCTGACT CTTCAAGAAT GCCATTCAAC AAGTATTTAT  
GGAGTACCTA
- 1301 CTATAATACA GTAGCTAACA TGTATTGAGC ACAGATTTTT  
TTTGGTAAAT
- 1351 CTGTGAGGAG CTAGGATATA TACTTGGTGA AACAAACCAG  
TATGTTCCCT
- 1401 GTTCTCTTGA GCTTCGACTC TTCTGTGCGC TACTGCTGCG  
CACTGCTTTT
- 1451 TCTACAGGCA TTACATCAAC TCCTAAGGGG TCCTCTGGGA  
TTAGTTATGC
- 1501 AGATATTAAA TCACCCGAAG AACTAACTT ACAGAAGACA  
CAACTCCTTC
- 1551 CCCAGTGATC ACTGTCATAA CCAGTGCTCT GCCGTATCCC  
ATCACTGAGG
- 1601 ACTGATGTTG ACTGACATCA TTTTCTTTAT CGTAATAAAC  
ATGTGGCTCT
- 1651 ATTAGCTGCA AGCTTTACCA AGTAATTGGC ATGACATCTG  
AGCACAGAAA
- 1701 TTAAGCCAAA AAACCAAAGC AAAACAAATA CATGGTGCTG  
AAATTAACCT

FIG.15B

- 1751 GATGCCAAGC CCAAGGCAGC TGATTCTGT GTATTGAAC  
TTACCCGAAA
- 1801 TCAGAGTCTA CACAGACGCC TACAGAAGTT TCAGGAAGAG  
CCAAGATGCA
- 1851 TTCAATTTGT AAGATATTTA TGGCCAACAA AGTAAGGTCA  
GGATTAGACT
- 1901 TCAGGCATTG ATAAGGCAGG CACTATCAGA AAGGTACGC  
CAACTAAGGG
- 1951 ACCCACAAAG CAGGCAGAGG TAATGCAGAA ATCTGTTTTG  
TTCCCATGAA
- 2001 ATCACCAATC AAGGCCTCCG TTCTTCTAAA GATTAGTCCA  
TCATCATTAG
- 2051 CAACTGAGAT CAAAGCACTC TTCCACTTTA CGTGATTAAA  
ATCAAACCTG
- 2101 TATCAGCAAG TTAAATGGTT CCATTCTGT GATTTTTCTA  
TTATTGAGG
- 2151 GGAGTTGGCA GAAGTTCCAT GTATATGGGA TCTTTACAGG  
TCAGATCTTG
- 2201 TTACAGGAAA TTTCAAAGGT TTGGGAGTGG GGAGGGAAAA  
AAGCTCAGTC
- 2251 AGTGAGGATC ATTCCACATT AGACTGGGGC AGAACTCTGC  
CAGGATTTAG
- 2301 GAATATTTTC AGAACAGATT TTAGATATTA TTTCTATCCA  
TATATTGAAA
- 2351 AGGAATACCA TTGTCAATCT TATTTTTTTA AAAGTACTCA  
GTGTAGAAAT
- 2401 CGCTAGCCCT TAATTCTTTT CCAGCTTTTC ATATTAATGT  
ATGCAGAGTC
- 2451 TCACCAAGCT CAAAGACACT GGTGCGGGGT GGAGGGTGCC  
ACAGGGAAAAG
- 2501 CTGTAGAAGG CAAGAAGACT CGAGAATCCC CCAGAGTTAT  
CTTCTCCAT
- 2551 AAAGACCATC AGAGTGCTTA ACTGAGCTGT TGGAGACTGT  
GAGGCATTTA
- 2601 GGAAAAAAAT AGCCCACTCA CATCATTCCT TGTAAGTCTT  
AAGTTCATTT

FIG.15C

- 2651 TCATTTTACG TGGAGGAAAA AAATTTAAAA AGCTATTAGT  
ATTTATTAAT
- 2701 GAATTTTACT GAGACATTTT TTAGAAATAT GCACTTCTAT  
ACTAGCAAGC
- 2751 TCTGTCTCTA AAATGCAAGT TGGCCTTTTG CTTGCCACAT  
TTCGCATTA
- 2801 AACTTCTATA TTAGCTTCAA AGGCTTTTAA TCTCAATGCG  
AACATTCTAC
- 2851 GGGATGTTCT TAGATGCCTT TAAAAAGGGG GCAAGATCTA  
ATTTTATTG
- 2901 AACCCCTACT TTCCAACTTT CACCATGACC CAGTACTAGA  
GATTAGGGCA
- 2951 CTTCAAAGCA TTGAAAAAAAA TCTACTGATA CTTACTTTCT  
TAGACAAGTA
- 3001 GTTCTTAGTT AACCACCAAT GGAAGTGGGT TCATTCTGAA  
TCCTGGAGGA
- 3051 GCTTCCTCGT GCCACCCAGT GTTTCTGGGC CCTCTGTGTG  
AGCAGCCAGG
- 3101 TGTGAGCTGT TTTAGAAGCA GCGTGTGGC TTCATCTCTC  
CCGTTTCCCA
- 3151 AAAGAACAAA GGATAAAGGT GACAGTCACA CTCTGGGGT  
AAAAAAGCA
- 3201 TTCCAGAACC ACTTCTCTTT ATGGGCACAA CAACAAAGAA  
GCTAAGTTCG
- 3251 CCTACCCAAA TGAAAGTAGG CTTTACAGTC AAGTACTTCT  
GTTGATTGCT
- 3301 AAATAACTTC ATTTTCTTGA AATAGAGCAA CTTTGAGTGA  
AATCTGCAAC
- 3351 ATGGATACCA TGTATGTAAG ATACTGCTGT ACAGAAGAGT  
TAAGGCTTAC
- 3401 AGTGCAAATG AGGCGTCAGC TTTGGGTGCT AAAATTAACA  
AGTCTAATAT
- 3451 TATTACCATC AATCAGGAAG AGATAATAAA TGTTTAAACA  
AACACAGCAG
- 3501 TCTGTATAAA AATACGTGTA TATTTACTCT TTCTGTGCAC  
GCTCTATAGC

FIG.15D

- 3551 ATAGGCAGGA GAGGCTTATG TGGCAGCACA AGCCAGGTGG  
GGATTTTGTA
- 3601 AAGAAGTGAT AAAACATTG TAAGTAATCC AAGTAGGAGA  
TATTAAGGCA
- 3651 CCAAAAGTAA CATGGCACCC AACACCCAAA AATAAAAAATA  
TGAAATATGA
- 3701 GTGTGAACTC TGAGTAGAGT ATGAAACACC ACAGAAAGTC  
TTAGAAATAG
- 3751 CTCTGGAGTG GCTCTCCCAG GACAGTTTCC AGTTGGCTGA  
ATAGTCTTTT
- 3801 GGCAGTGATG TTCTACTTCT TCACATTCAT CTAACAAAAA  
AAAAAAAAA

FIG.15E

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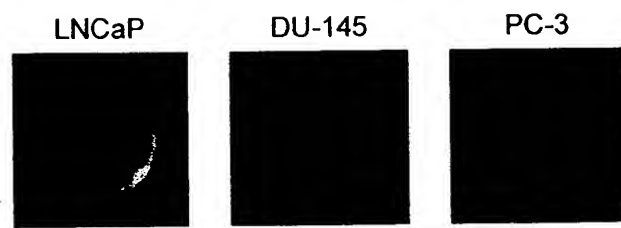


FIG.16A FIG.16B FIG.16C

Secreted and Cellular PCTA-1

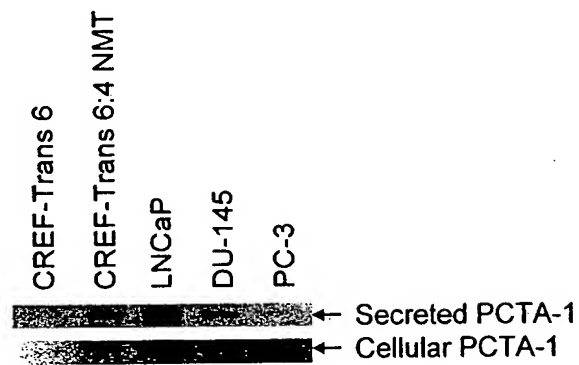


FIG.16D



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FIG. 17A



FIG. 17B



FIG. 17C



FIG. 17D

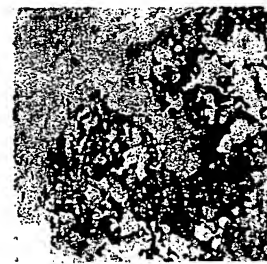


FIG. 17E

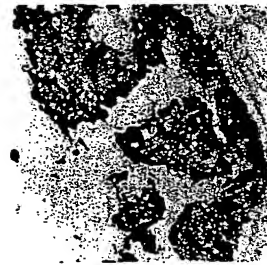


FIG. 17F



FIG. 17G

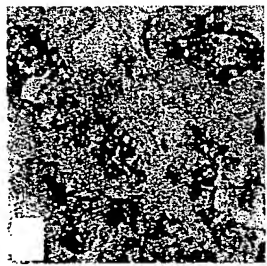


FIG. 17H

**FIGURE 18A**

54	ATG	ATG	TTG	TCC	TTA	AAC	AAC	CTA	CAG	AAT	ATC	ATC	TAT	AAC	CCG	GTA	ATC	CCG	TTT	GTT
	M	ACC	L	S	L	N	N	L	Q	N	I	I	Y	N	P	V	I	P	F	V
114	GGC	ACC	ATT	CCT	GAT	CAG	CTG	GAT	CCT	GGA	ACT	TTG	ATT	GTG	ATA	CTG	GGG	CAT	GTT	CCT
	G	T	I	P	D	Q	L	D	P	G	T	L	I	V	I	R	G	H	V	P
174	AGT	GAC	GAC	GAC	AGA	TTT	CTG	CTG	GAT	CTG	CAG	AAT	GCG	AGC	GTG	AAA	CCT	CGA	GCC	
	S	D	A	D	R	F	Q	V	D	L	Q	N	G	S	S	V	K	P	R	A
234	GAT	GTG	GCC	TTT	CAT	TTT	AAT	CCT	CCT	TTT	AAA	AGG	GCC	TGC	ATT	GTT	TGC	AAT	ACT	
	D	V	A	F	H	F	N	P	R	F	K	R	A	G	C	I	V	C	N	T
294	TTG	ATA	AAT	GAA	AAA	TGG	GGA	CGG	GAA	ATC	ACC	TAT	GAC	ACG	CCT	TTT	AAA	AGA	GAA	
	L	I	N	E	K	W	G	R	E	E	I	T	Y	D	T	P	F	K	R	E
354	AAG	TCT	TTT	GAG	ATC	CTG	ATT	GTG	CTG	AAG	GAC	AAA	TTT	CAG	GTG	GCT	GTA	AAT	GGA	
	K	S	F	E	I	V	I	M	V	L	K	D	K	F	Q	V	A	V	N	C
414	AAA	CAT	ACT	CTG	CTC	TAT	GGC	CAC	AGG	ATC	GGC	CCA	GAG	AAA	ATA	GAC	ACT	CTG	GGC	ATT
	K	H	T	L	L	Y	G	H	R	I	G	P	E	K	I	D	T	L	G	I
474	TAT	GGC	AAA	GTG	AAT	ATT	CAC	TCA	ATT	CGT	TTT	AGC	TTT	AGC	TGC	GAC	TTA	CAA	AGT	ACC
	Y	G	K	V	N	I	H	S	I	G	F	S	F	S	S	D	L	Q	S	T
534	CAA	GCA	TCT	AGT	CTG	GAA	CTG	ACA	GAG	ATA	GTT	AGA	GAA	AAT	GTT	CCA	AAT	TCT	GGC	ACT
	Q	A	S	S	L	E	L	T	E	I	V	R	E	N	V	P	K	S	G	T
594	CCC	GAC	CTT	AGC	CTG	CCA	TTT	GCT	GCA	AGG	TTG	AAC	ACC	CCC	ATG	GGC	CCT	GGA	CGA	ACT
	P	Q	L	S	L	P	F	A	A	R	L	N	T	P	M	G	P	G	R	T
654	GTC	GTC	GTT	CAA	GGA	GAA	GTG	AAT	GCA	AAT	GCC	AAA	AGC	TTT	AAT	GTT	GAC	CTA	CTA	GCA
	V	V	V	V	G	E	V	N	A	N	A	K	S	F	N	V	D	L	L	A
714	GGA	AAA	TCA	AAG	GAT	ATT	GCT	CTA	CAC	TTG	AAC	CCA	CGC	CTG	AAT	ATT	AAA	GCA	TTT	GTA
	G	K	S	K	D	I	A	L	H	L	N	P	R	L	N	I	K	A	F	V
774	AGA	AAT	TCT	TTT	CTT	CAG	GAG	TCC	TGG	GGA	GAA	GAG	AGA	AAT	ATT	ACC	TCT	TTT	CTT	GCA
	R	N	S	F	L	Q	E	S	W	G	E	E	E	R	N	I	T	S	F	P
834	TTT	AGT	CCT	GGG	ATG	TAC	TTT	GAG	ATG	ATA	ATT	TGT	GAT	GTT	AGA	GAA	TTT	AAG	GAT	GTT
	F	S	P	G	M	Y	F	E	M	I	I	Y	C	D	V	R	E	F	K	V
894	GCA	GTA	AAT	GGC	GTA	CAC	AGC	CTG	GAC	TAC	AAA	CAG	AGA	TTT	AAA	GAG	CTC	AGT	AGT	ATT
	A	V	N	G	V	H	S	L	E	Y	K	H	R	F	K	E	L	S	S	I
954	GAC	ACG	CTG	GAA	ATT	AAT	GGA	GAC	ATC	CAC	TTA	CTG	GAA	CTA	AGG	AGC	TGG	TAG		
	D	T	L	E	I	N	G	D	I	H	L	L	L	E	V	R	S	W		

[illegible][illegible]

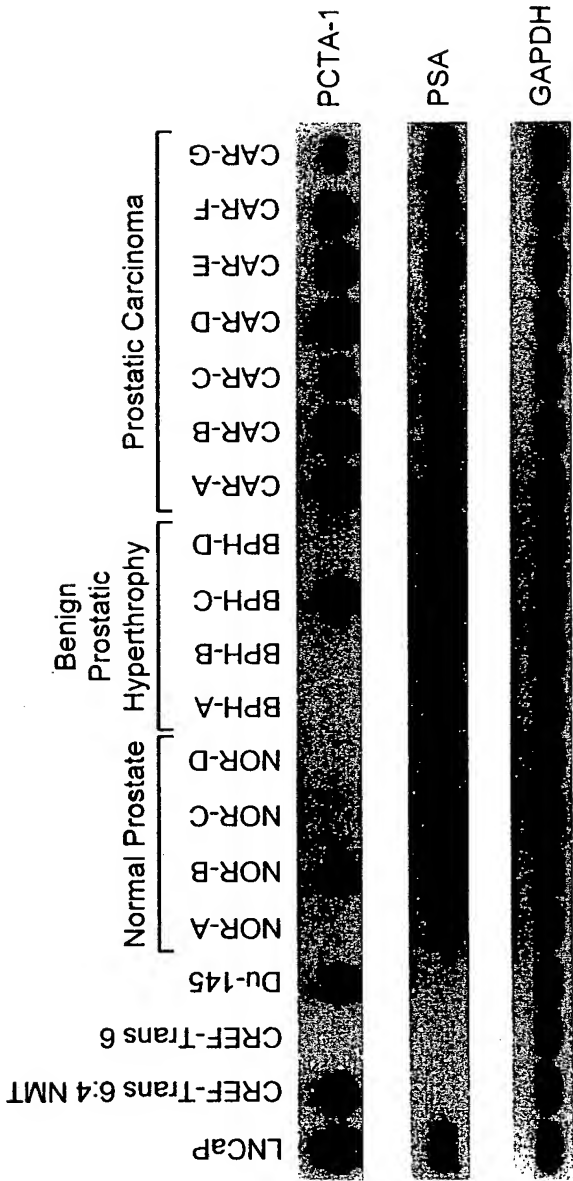


FIG.19